nano-protein complexes (DNase I, BSA, GFP and Hand2) with the charge force, hydrogen bonding and hydrophobic effect between protein and NG nano-particles to test the optimal transfection condition. In addition, with the help of the growth factors and small molecular compounds, we engage to induce hBMSCs differentiating into (protein induced) CPCs. After incubating for 1d, 3d, 8d, 5d, we observe the cells' morphological changes respectively, the detect the relative mRNA and proteins' expression level as piCPCs marker.

RESULTS Diameter and Zeta potential detection, immunofluorescence and Wb reveal the optimal Mol number ration between particle and protein is 1:1. TEM directly shows nano-protein complexes 'original appearance in spherical shape, AGE and SDS-PAGE electrophoresis indicate nano-paiticles also can protect protein from degradation. The nano-modifid proteins can be imported into cytoplasm and nucleus depends on the protein's characteristics, and there is no influence on protein activity. After transfected by nano-GHMT complexes, mRNA expression level of piCPCs markers (Tbx5, Isl-1, Nkx2.5) are significant up-regulated in induced hBMSCs, so as the protein expression level of sm-MHC, α-SMA, CD31, which represent three myocardial lineages of piCPCs: cardiomyocyte, smooth muscle cell, and endothelial cell.

CONCLUSIONS Nano-protein technology is a excellent cell-reprogramming method with good clinical application prospects. We also find that only 4 modified Cardiac specific transcription factors can induce hBMSCs differentiating into CPCs, which provide new source for cell therapy of myocardial injury.

GW26-e2364

Flotillin-2 Gene is Associated With Coronary Artery Disease in Chinese Han Population

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OBJECTIVES In human, vesicular endocytosis is an efficient way of dietary cholesterol absorption. Flotillins proteins included Flotillin-1, Flotillin-2 are considered to be the components of lipid rafts and are commonly used as marker proteins for lipid microdomains. Therefore, we investigated the association between the human flotillin-2 gene polymorphism and coronary artery disease (CAD) in Chinese Han population.

METHODS We recruited an independent case-control study (307 CAD patients and 441 control subjects). All of the CAD patients and control subjects were genotyped for the same 3 single nucleotide polymorphisms (SNPs) (rs10205, rs3816848 andrs8081659) of flotillin-2 gene by a real-time PCR instrument.

RESULTS The genotypic distribution of the 3 SNPs for flotillin-2 gene was significantly different between CAD patients and control subjects (all $P< 0.05$). For rs10205, the frequency of the TT genotype was significantly higher in patients with CAD than that in controls (8.8% vs. 4.3%; $P=0.023$). For rs3816848, the frequency of the GG genotype was significantly higher in patients with CAD than that in controls (25.7% vs. 12.9%; $P<0.001$). For rs8081659, the frequency of the CC genotype was significantly lower in patients with CAD than that in controls (45.9% vs. 54.9%; $P=0.002$). There were significant differences in the plasma levels of TC among different genotypes in CAD group and total group. For rs3816848, CAD patients with GG genotype had a higher level of TC than that with AG or AA genotype ($P< 0.001$). For rs8081659, CAD patients with TT genotype had a higher level of TC than that with CT or CC genotype ($P< 0.001$). Multiple logistic regression analysis showed that GG genotype of rs3816848 was an independent risk factor for CAD (OR=1.786; 95% CI=1.099-2.902; $P=0.019$).

CONCLUSIONS There was a strong association between the flotillin-2 gene and CAD in Chinese Han population. People with GG genotype of rs3816848 may have a higher risk of CAD. Moreover, the plasma levels of TC were significant different among the different genotypes of rs3816848 and rs8081659 between CAD group and total group.

GW26-e2365

Association of C5aR1 Genetic Polymorphisms With Pathogenesis and Prognosis of Coronary Artery Disease in Xinjiang Han and Uygur Population

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OBJECTIVES Complement 5a receptor (C5aR) was demonstrated a receptor of complement 5a (C5a) which is involved in many inflammatory diseases. The functional responses attributed to C5a results from its interaction with its receptors C5aR, which stimulates food intake, plays a role in increasing the inflammatory response in adipose tissue as well as the cardiovascular and neural systems. However, there are unknown associations between the SNPs of C5aR1 gene and coronary artery disease (CAD). For different genotypes for CAD group with 2-5 years of follow-up, to observe different genotype relationship with prognosis of CAD major adverse cardiac events (MACE).

METHODS We examined the role of the tagging single nucleotide polymorphisms (SNPs) of C5aR1 gene for CAD using two independent case-control studies: one was in the Han population (784 CAD patients and 703 control subjects) and the other was in the Uygur population (580 CAD patients and 886 control subjects).

RESULTS rs10853784 polymorphic was association with CAD in Han population (OR=1.430, 95% CI: 1.087 ~ 1.882, P =0.011), the haplotype A-C-T built by C5aR1 tag SNPs is a protective marker for CAD and A-T-C is a risk factor for CAD in Han population. A-C-C is a risk factor for CAD and A-C-T is a protective marker for CAD in Uygur population. By 2-5 years of follow-up, For rs10853784 gene polymorphism has nothing to do with the prognosis of CAD.

CONCLUSIONS The results of this study indicate that rs10853784 of C5aR1 gene are associated with CAD in Xinjiang Han and Uygur population. But has nothing to do with the prognosis of CAD.

GW26-e2368

Association of C5L2 Genetic Polymorphisms and Prognosis of Coronary Artery Disease in Xinjiang Han and Uygur Population, China

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OBJECTIVES C5aR-like receptor 2 (C5L2) has been identified as a receptor for the inflammatory factor Complement 5a(C5a) and acylation-stimulating protein (ASP). ASP binding to C5L2 leading to a net accumulation of TG stores and glucose transporter. The aim of the present study is to evaluate the association of the SNPs of C5L2 gene and their association with coronary artery disease (CAD). For different genotypes for CAD group with 2-5 years of follow-up, to observe different genotype relationship with prognosis of CAD major adverse cardiac events (MACE).

METHODS We examined the role of the tagging single nucleotide polymorphisms (SNPs)of C5L2 gene for CAD using two independent case-control studies: one was in the Han population (784 CAD patients and 703 control subjects) and the other was in the Uygur population (580 CAD patients and 886 control subjects).

RESULTS There was significant difference in genotype distributions of rs2972607 and rs8112962 between CAD patients and control subjects. The tag SNP rs2972607 dominant model was association with CAD in Han and Uygur population. After adjustment of confounding factors, the difference remained significant in the Han group (P =0.034, OR=1.401, 95% CI=1.026~1.914 and P =0.01, OR=1.408, 95% CI=1.087- 1.824, respectively). the rs8112962 dominant model was association with CAD in Han population (P =0.014, OR=1.541, 95% CI=1.039~2.172); By 2-5 years of follow-up, we find in the Han population, risk of a the occurrence of MACE event was significantly higher in C5L2 gene rs2972607 AA genotype the occurrence of MACE event with AA genotype increased 2.122 times versus wild CC genotype carriers (HR = 2.122, 95% CI: 1.302-6.113), but not found in the Uygur patients. rs2972607 polymorphism was associated with MACE related events.

CONCLUSIONS The results of this study indicate that the rs2972607 and rs8112962 of C5L2 gene are associated with CAD in Han population of China. In the Han population, rs2972607 of C5L2 gene was associated with MACE related events.

GW26-e2377

The Immunosuppressant Protosappanin A Promotes Dendritic Cell-Mediated Expansion of Alloantigen-Specific Tregs and Prolongs Allograft Survival in Rats

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OBJECTIVES Protosappanin A (PrA), an immunosuppressive ingredient of the medicinal herb Caesalpinia sappan L, prolongs heart